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Research Article

Occurrence and composition of Phlebotomine sandflies (Diptera, Psychodidae) in selected areas along the East Africa Great Rift Valley ecosystem, Tanzania

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Abstract

Sandflies are dipterans of medical significance, well-known for transmitting *Leishmania* parasite. This study investigated the occurrence, composition and distribution of sandflies. Sandflies were collected for three consecutive nights each week at each sampling point using CDC miniature light traps, sticky traps and manual aspiration. Captured sandflies were morphologically identified, based on head structure and terminalia, following standard keys. A generalised linear model was used to determine the effects of explanatory variables on sandfly abundance. Shannon-wiener and Jaccard's similarity indices were utilised to calculate species diversity and community similarity, respectively. A total of 586 Phlebotomine sandflies were collected, comprising eight species; *Sergentomyia freetownensis* (38.74%), *Se. antennata* (49.49%), *Se. schwetzi* (4.61%), *Se. bedfordi* (3.75%), *Se. adleri* (1.19%), *Grassomyia squamipleuris* (0.68%), *Phlebotomus martini* (0.85%) and *Ph. vansomerenae* (0.68%). Sandfly abundance was significantly influenced by habitat type (X^2 = 71.6, df = 2, P < 0.001), altitudinal range (X^2 = 46.85, df = 2, P < 0.001), average temperature (X^2 = 39.16, df = 1, P < 0.001) and average relative humidity (X^2 = 41.03, df = 1, P < 0.001). Sandfly diversity was higher in farmland (H' = 1.149) and at mid-altitude areas (H' = 1.079). The presence of competent and susceptible vectors species in the study villages underscores the necessity for surveillance, including vectorial capacity and bloodmeal sources as fundamental factors in incriminating the vector in areas considered non-endemic.

Key words: Abundance, distribution, diversity, vector

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Introduction

Vector-borne diseases (VBDs), such as dengue, Chagas disease, human African trypanosomiasis, leishmaniasis and malaria pose a significant burden of morbidity and mortality worldwide (Campbell-Lendrum et al. 2015; Wilson et al. 2020; Nigusie et al. 2021). Nearly 80% of the world's population is threatened by VBDs; however, less developed countries, primarily in Africa and Asia, suffer

the greatest impact. Most of these diseases are classified as neglected tropical diseases (NTDs) (Costa et al. 2019; Gaudêncio et al. 2020; Wilson et al. 2020). They are not transmitted directly amongst humans; instead, transmission requires favourable ecological and environmental interactions involving vectors, reservoir hosts, climate, pathogens and susceptible human populations (Ready 2010; Savi 2014; de Araujo-Pereira et al. 2020; Chala and Hamde 2021).

Several vector-borne pathogens have colonised new regions in the past few decades, while an equivalent number of endemic diseases have shown increased incidences (Desjeux 2001; Grifferty et al. 2021; WHO 2021). Overall, the transmission and burden of VBDs are potentially increasing, consequent to human population growth, globalisation, trade, travel and close interactions between domestic and wild fauna, amongst other factors (Schmidt et al. 2013; Booth 2020; Chala and Hamde 2021).

Leishmaniasis, caused by protozoan parasites of the genus *Leishmania*, is endemic in nearly 100 countries worldwide, where approximately 1.6 billion people are at risk and there are 12 million cases of infection (Grifferty et al. 2021; WHO 2021). Overall, leishmaniasis accounts for the ninth-largest disease burden amongst infectious diseases (Berry and Berrang-Ford 2016), due to its complex zoonotic transmission cycles involving multiple hosts, such as canids, rodents, marsupials, lizards, hyraxes and humans (Steverding 2017; Mendoza-Roldan et al. 2021).

The disease disproportionately affects underserved populations with limited access to quality health services, disease education, preventative tools and other infrastructures (Scarpini et al. 2022). There are generally four main clinical forms of the disease: cutaneous leishmaniasis (CL), visceral leishmaniasis (VL, also known as kala-azar), post-kala-azar dermal leishmaniasis (PKDL) and mucocutaneous leishmaniasis (MCL). The first three forms often occur in the East African Region (Malaria Consortium 2010; WHO 2021).

Leishmaniasis is transmitted through the infective bites of haematophagous female sandflies belonging to the *Phlebotomus* and *Lutzomyia* genera (Maroli et al. 2013; Jones and Welburn 2021). For a species of sandfly to be considered a competent vector of *Leishmania* spp., particularly the zoonotic ones, it must meet five conditions: be anthropophilic; feed from reservoir hosts in cycles of zoonotic transmission; be able to be infected in nature with the *Leishmania* species that infects humans; harbour the complete development stages of the parasite until it becomes infective; and be capable of transmitting the parasite through its bite (Azami-Conesa et al. 2021). The most commonly encountered vector species of sandflies in East Africa include *Phlebotomus martini*, *Ph. orientalis*, *Ph. pedifer*, *Ph. vansomerenae*, *Ph. guggisbergi* and *Ph. duboscqi* (Malaria Consortium 2010; WHO 2021).

Tanzania is part of the East African great rift valley ecosystem, where leishmaniasis is mostly prevalent. Competent sandfly vectors are present in these areas and possibly elsewhere in the country, posing a significant risk for disease emergence and spread (Ready 2010; Ballart et al. 2014). The risk and burden of disease transmission are likely increasing due to multiple interacting factors, such as climate change, increased human and animal population mobility and forest encroachment (Desjeux 2001; Booth 2020). Human leishmaniasis is a climate-sensitive disease, as the distribution and abundance of sandflies are

strongly influenced by meteorological, environmental and demographic factors (Ballart et al. 2014; Carvalho et al. 2015).

Despite this underlining risk and burden, critical information necessary for enhancing disease surveillance and control is grossly lacking. Moreover, only one entomological survey has been conducted in the country over the past decade (Clark et al. 2013). This situation warrants immediate studies to understand, amongst other factors, the ecology and population dynamics of sandfly vectors, as well as their interactions with parasites, hosts and environment, let alone the epidemiology of *Leishmania* parasites. This study aimed to investigate the species occurrence, composition, distribution and abundance of sandfly vectors along the East Africa Great Rift Valley ecosystem, specifically in the Manyara and Arusha Regions of Tanzania. The findings provide essential baseline data for guiding future investigations and strengthening the vector surveillance strategies.

Materials and methods

Study area

The study was conducted in selected areas along the Eastern Africa Great Rift Valley ecosystem in Arusha and Manyara regions of Tanzania. Arusha Region is located at latitude 2°S to 6°S and longitude 35°E to 38°E with an elevation of 1400 m above sea level. Manyara is located at latitude 3°40'S to 6°S and longitude 33°E to 38°E and its elevation is variable. The mean annual rainfall ranges from 800 mm to 1200 mm and 450 mm to 1200 mm in Arusha and Manyara, respectively. Both regions experience a bimodal rainfall pattern. In Arusha, the long rainy season runs from March to May and short rainy season runs from October to January, while, in Manyara Region, the long rainy season runs from January to May and short rainy season runs from October to December. The dry season runs from June to October in both regions. Overall, the temperature varies from 13 °C to 28 °C in Arusha Region and 13 °C to 33 °C in Manyara Region (PO-RALG 2016a, 2016b). These regions are generally considered semi-arid. The main economic activities in both regions include tourism, semi-pastoralism and subsistence farming. In both regions, human-wildlife interactions are obvious due to their proximity to national parks and other forms of natural reserves (PO-RALG 2016a, 2016b).

Study design

A cross-sectional study design was used, one district from each region being selected, with two wards sampled from each district. The selected wards included Migungani and Selela wards from Monduli District in the Arusha Region and Magugu and Dareda wards from Babati District in the Manyara Region (Fig. 1). Simply, district and ward selection were based on their semi-arid nature. Additionally, six villages (Loto, Seloto, Magugu, Kigongoni, Migungani B and Selela) were purposefully selected, based on their proximity to protected areas, geographical features (such as elevation) and human mobility pattern (PO-RALG 2016a, 2016b). The locations of each trapping site are detailed in Suppl. material 1.

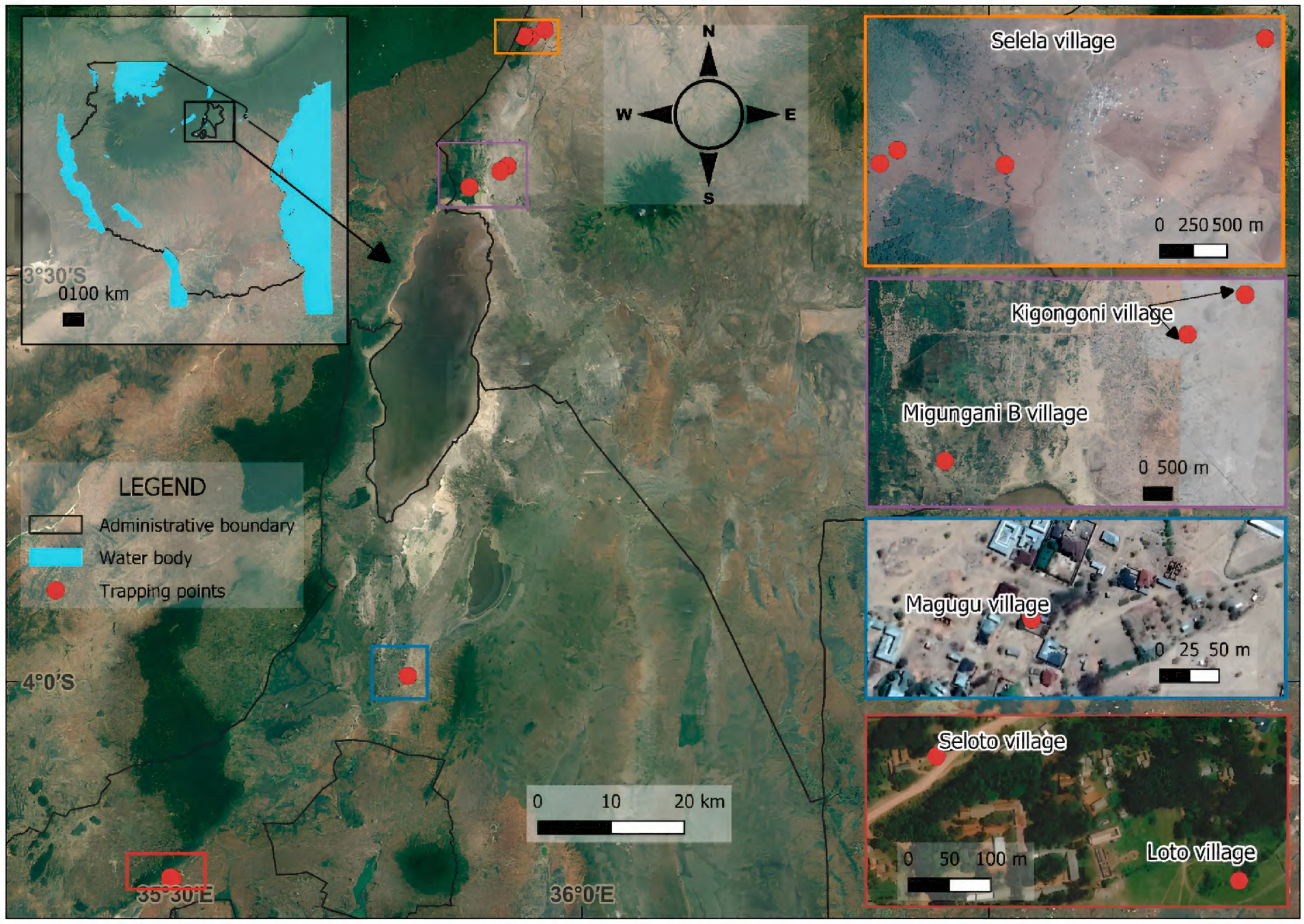

Figure 1. Map showing study villages along the East Africa Great Rift Valley ecosystem, Babati and Monduli districts, Tanzania. The map was developed on February 2024 using QGIS software version 3.26.1.

Sandflies collection

Sandflies were collected during the late wet season, from April to May 2022, using CDC miniature light traps (John W. Hock Company, USA), sticky traps (20 × 29 cm sheets of paper covered with 10 ml of castor oil) and manual collection with aspirators (Fig. 2). The CDC light traps, powered by 6-V rechargeable batteries, were placed in peridomicile areas (10–15 m from human dwelling and cattle shed), agricultural areas (farmland) and human-wildlife interfaces (HWIs, buffer zone). The traps were positioned 200 m apart, hung 0.3 m above the ground and operated from 1800 hr to 0600 hr for three consecutive nights each week at a single point before being transferred to another site (Kasili et al. 2010). Sticky traps were placed in the diurnal resting spots of sandflies, notably near termite hills, rock crevices, house cracks and thickets and were collected after 2 days. Number and position of sticky traps were varied, based on the nature of the resting spots, some being rolled and inserted within rock crevices and other placed vertically (Fig. 2A, B). Manual collections were conducted in the same vector resting locations during early morning and evening, using a Mosquito Aspirator w/HEPA filter – Acrylic pipe – 30 cm LI.MR.29 (Senanayake et al. 2015).

Once collected, sandflies were sorted by sex using external morphological characteristics under a stereomicroscope and then placed in cryovials containing 70% ethanol. Sandflies captured on sticky trap were removed with an

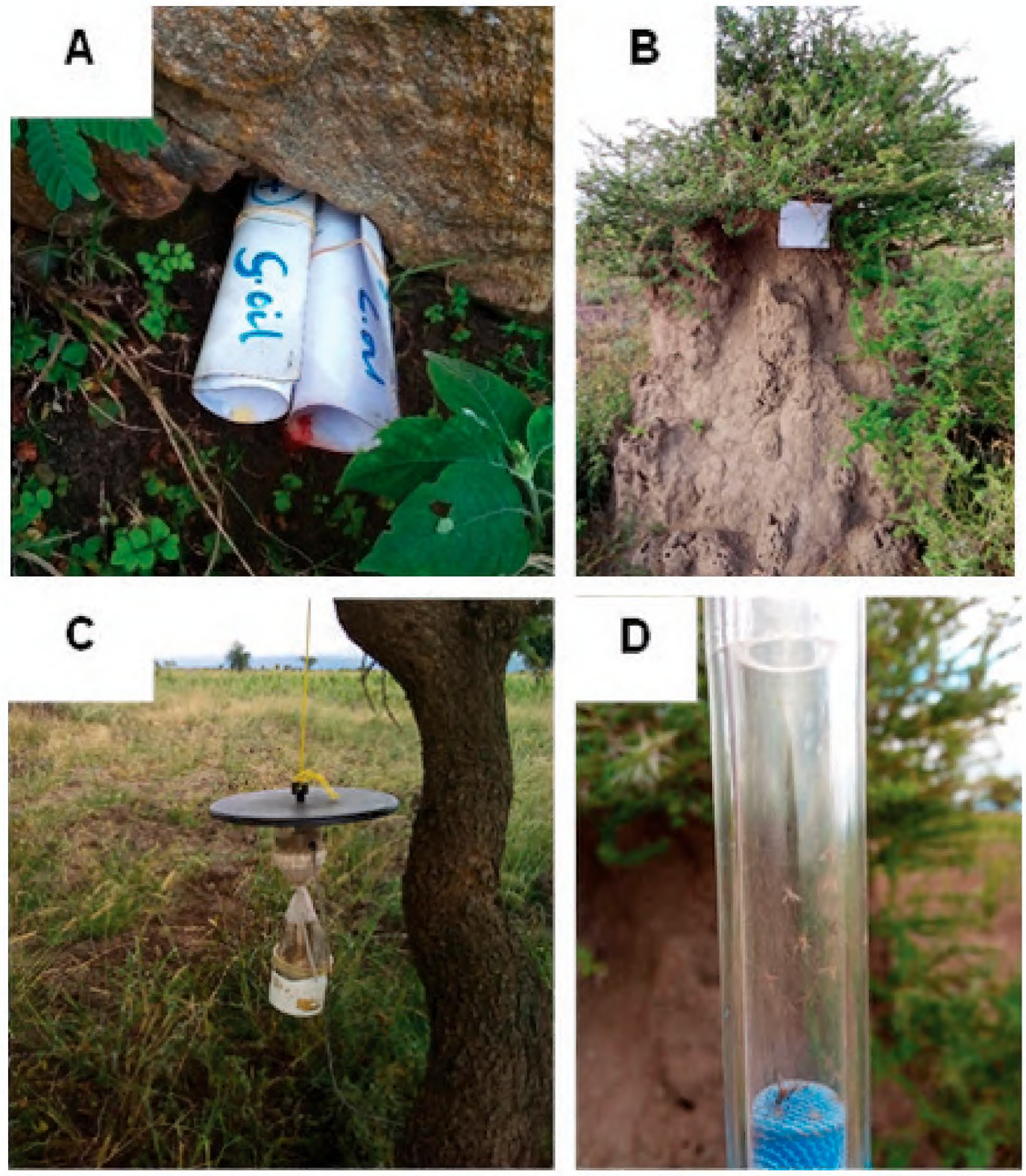

Figure 2. A–D. Different traps used during sandflies collection. **A.** Sticky trap covered with castor oil, coiled and placed under rock crevices; **B.** Sticky trap placed on termite hill with acacia vegetation; **C.** CDC miniature light trap hung 0.3 m above the ground (closed in the morning); **D.** Sandflies collected via aspirator.

entomological brush and fixed in 95% ethanol for 2 days to dissolve the oil (González et al. 2017), before being stored as described above until morphological identification.

Sandflies species identification

Sandflies were clarified according to Costa et al. (2019), with modifications. Specimens were submerged in a 10% sodium hydroxide solution for 2 hours, then placed in 10% acetic acid for 20 minutes to neutralise the alkalinity. Afterwards, specimens were washed in distilled water three times for 15 minutes each and then immersed in lactophenol for 24 hours prior to mounting on a microscope slide using DPX mountant. Morphological identification was based on head structure and terminalia, using identification keys (Kirk and Lewis 1948, 1951; Abonnenc 1972; Lewis 1982) (Figs 3, 4). The taxonomic ranking follows the system proposed by Kvifte and Wagner (2017) for generic classification of *Grassomyia* and Marcondes (2007) for the generic abbreviation system.

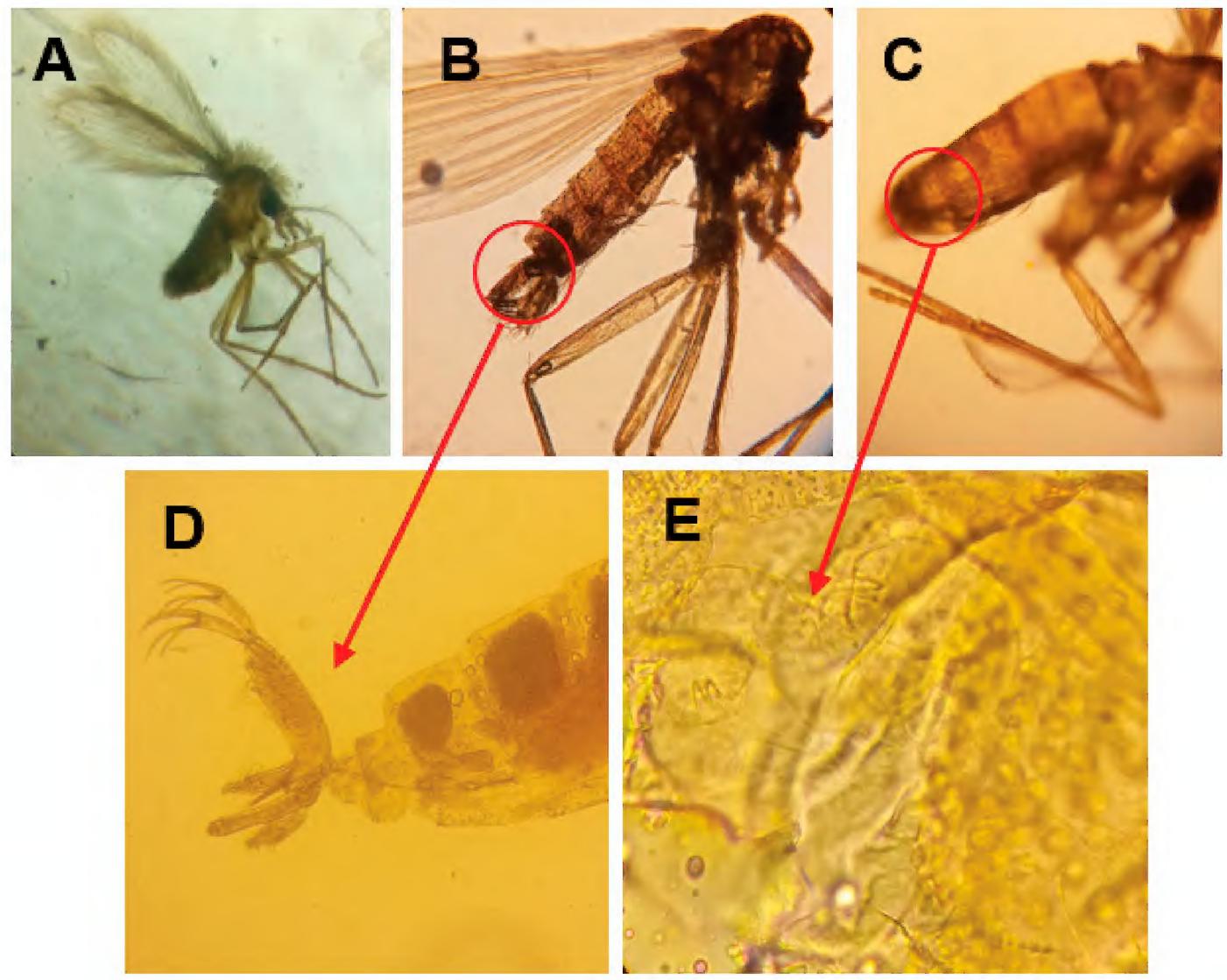

Figure 3. A–E. Structure of sandflies. **A.** Phlebotomine sandfly; **B.** Male terminalia; **C.** Female terminalia; **D.** Male terminal structures (*Sergentomyia*); **E.** Spermatheca (*Sergentomyia*).

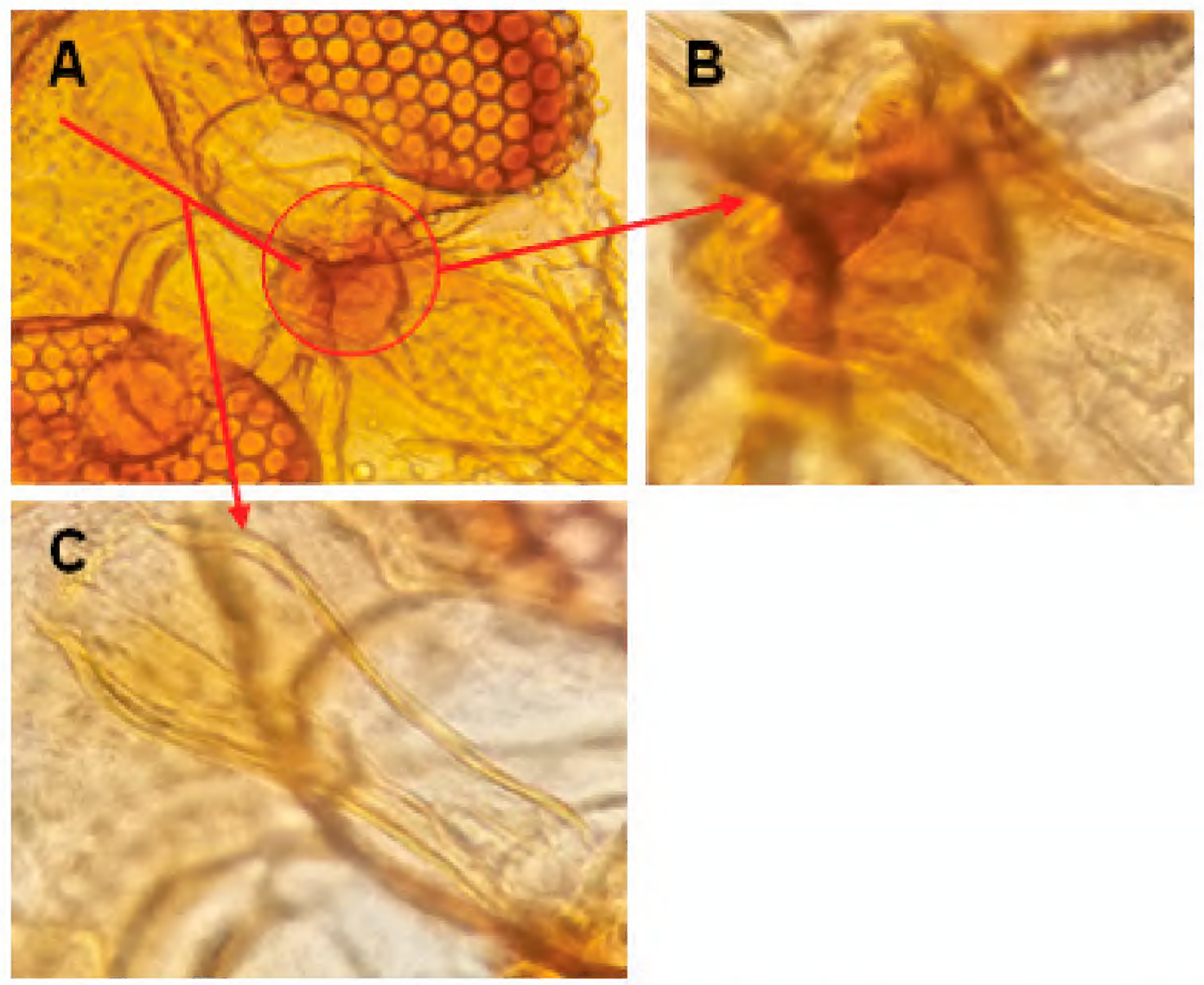

Figure 4. A–C. Phlebotomine sandfly head structure. **A.** Head structure; **B.** Cibarium chamber; **C.** Pharynx (*Sergentomyia*).

Collection of meteorological parameters

Data loggers HTC-1 with temperature and humidity meter were installed at each sampling location to record the maximum and minimum temperature and relative humidity (%RH) during the sampling periods (Talbi et al. 2020). Additionally, altitude was recorded at each sampling point following calibration of the barometric altimeter, using GARMIN-GPSMAP65S device.

Data analysis

Data were cleaned and organised in Microsoft Excel version 2019. The spatial distribution of sand flies was estimated according to species by the pattern of occurrence (C%), as defined in Equation 1: sporadic (C = 0–20%), infrequent (C = 20.1–40%), moderate (C = 40.1–60%), frequent (C = 60.1–80%) or constant (C = 80.1–100%) (Kabbout et al. 2016). Predominant sandfly species were estimated by relative abundance (RA%), calculated as the ratio of the number of specimens for each species to the total number of specimens caught, multiplied by 100. Ecological indices were calculated as described by Yahaghi et al. (2022). The Shannon-Wiener diversity index is expressed in Equation 2, the evenness index in Equation 3 and Jaccard's similarity index in Equation 4.

$$C = n / N \quad (1)$$

where n = number of sites positive for sand flies of each species; N = total number of positive sites.

$$H' = - [\sum (Pi * lnPi)] \quad (2)$$

where 'p_i' can be calculated by dividing n_i, the number of individuals of each species, by N, the total number of collected individuals.

$$E = H' / \ln S \quad (3)$$

where H' is the diversity index, 'ln' is natural logarithm and 'S' is the number of collected species.

$$Sj = a / (a + b + c) \quad (4)$$

where 'a' denotes the number of species found in both biotopes, 'b' is the number of species found in the first biotope and 'c' biotope is the number of species in the second biotope.

The effect of different explanatory variables (habitats [farmland, peridomicile, HWI], altitude range [mid, low, high], average RH, average temperature) on the abundance of sandflies was assessed by generalised linear model (GLM) under a Poisson family, available in MASS package (R version 3.4.3). Non-normality of count data was assessed using the Shapiro-Wilk test prior to analysis.

Additionally, the significance of predictor variables with more than two categories was tested using the ANOVA function in the car package. Statistical tests were considered significant when the p-value was < 0.05.

Study limitation

This study employed a cross-sectional design, primarily focusing on piloting data regarding the occurrence and composition of sandflies in the surveyed villages. However, this design is limited in its ability to capture temporal variations. Consequently, further longitudinal studies are necessary to assess spatial-temporal variations, as well as to conduct surveillance on vectorial capacity and bloodmeal sources.

Results

Species composition and abundance

A total of 586 phlebotomine sandflies were collected throughout the survey from six villages along the East Africa Great Rift Valley ecosystem. Of the collected flies, 432 (73.7%) were males and 154 (26.3%) were females. The samples comprised three genera and eight species. Of these, 573 (97.78%) belonged to the genus *Sergentomyia*; *Se. freetownensis* (n = 227, 38.74%), *Se. antennata* (n = 290, 49.49%), *Se. schwetzi* (n = 27, 4.61%), *Se. bedfordi* (n = 22, 3.75%), *Se. adleri* (n = 7, 1.19%). Additionally, 9 (1.54%) belonged to genus *Phlebotomus*; *P. martini* (n = 5, 0.85%) and *P. vansomerenae* (n = 4, 0.68%). Finally, 4 (0.68%) belonged to genus *Grassomyia*; *Gr. squamipleuris* (Table 1).

The most predominant phlebotomine sandflies species were *Se. antennata* (49.49%), followed by *Se. freetownensis* (38.74%). Unlike the former, the latter species was collected in all surveyed villages. On the other hand, the least dominant species were *Gr. squamipleuris* (0.68%) and *Ph. vansomerenae* (0.68%), both of which were collected from a single village. The number of phlebotomine sandfly species for each surveyed village is reported in Suppl. material 1.

The sandflies abundance was significantly influenced by habitat type (X^2 = 71.6, df = 2, P < 0.001), altitudinal range (X^2 = 46.85, df = 2, P < 0.001),

Table 1. Species composition and relative abundance of sandflies.

Genus	Species	Male		Female		Total	Relative abundance (%)
		n	(%)	n	(%)	N	
Phlebotomus	*Ph. martini*	5	100.00	0	0.00	5	0.85
	Ph. vansomerenae	4	100.00	0	0.00	4	0.68
Sergentomyia	*Se. freetownensis*	176	77.53	51	22.47	227	38.74
	Se. antennata	219	75.52	71	24.48	290	49.49
	Se. schwetzi	24	88.89	3	11.11	27	4.61
	Se. adleri	0	0.00	7	100.00	7	1.19
	Se. bedfordi	0	0.00	22	100.00	22	3.75
Grassomyia	*Gr. squamipleuris*	4	100.00	0	0.00	4	0.68
	Total (8 species)	432	73.72	154	26.28	586	100.00

average temperature (X^2 = 39.16, df = 1, P < 0.001) and average Relative Humidity (X^2 = 41.03, df = 1, P < 0.001). Across habitats, the abundance of sandflies was 295 (50.34%) in farmland, 252 (43%) in peridomicile and 39 (6.66%) at the human-wildlife interface (HWI). The model (estimate ± SE, p-value) reveals that peridomicile (-0.96 ± 0.12, P < 0.001) and HWI (-0.9 ± 0.17, P < 0.001) were significantly associated with a decrease in sandflies abundance relative to farmland. This indicates that farmland provides an ideal environment for the perpetuation of sandflies compared to peridomicile and HWI.

Furthermore, altitudinal levels impact the composition and abundance of sandflies, with the highest abundance (451) found at mid-altitude, followed by low-altitude (133) and least at high-altitude (2). The model indicated that low-altitude (2.93 ± 0.72, P < 0.001) and mid-altitude (3.42 ± 0.76, P < 0.001) were significantly associated with an increase in sandflies abundance. In contrast, high-altitude areas were characterised by cooler temperature and high humidity, which likely to impede sandflies abundance.

Spatial distribution of sandflies

All surveyed villages exhibited the presence of at least one phlebotomine sandfly species. The occurrence pattern revealed that *Sergentomyia freetownensis* was the most constant species with the broad geographical distribution (C = 100%). This species was caught in all surveyed villages. *Sergentomyia antennata*, *Se. schwetzi* and *Se. bedfordi* showed a moderate occurrence pattern (C = 50%) and were caught in three villages. *Phlebotomus martini* had an infrequent occurrence pattern (C = 33%), while *Se. adleri*, *Gr. squamipleuris* and *Ph. vansomerenae* were the least common species, exhibiting narrow geographical distribution. The latter three species had a sporadic occurrence pattern (C = 16%). The number and distribution of sandfly species in each village and habitat are reported in Suppl. material 1. The genus *Phlebotomus* was recorded only in Kigongoni and Selela Villages, while the genus *Sergentomyia* was found in all surveyed villages.

Diversity and similarity indices

Sandflies species richness varied slightly across villages and habitats. Overall, sandflies diversity was three-fold higher in Selela (H' 1.13) and two-fold higher in Kigongoni (H' 0.96) compared to Magugu (H' 0.43). However, no diversity was observed in Migungani B, Loto and Seloto (Table 2). Across habitats, farmland exhibited high diversity (H' 1.15), followed by peridomicile (H' 1.10), with the least diversity at HWI (H' 0.43). At different altitudinal levels, the mid-altitude area had higher diversity (H' 1.1) than the low-altitude area (H' 0.7), while there was no diversity in the high-altitude area.

The sandflies community similarity coefficient was highest (80%) between the Magugu and Selela Villages and lowest (50%) between Kigongoni and Magugu. The similarity coefficient between Kigongoni and Selela was 62.5%. Across habitats, the Jaccard's similarity coefficient was high (75%) between farmland and peridomicile. In contrast, the coefficients for farmland versus HWI and peridomicile versus HWI were both 42.8%. Moreover, the mid-altitude

and low-altitude areas exhibited a community similarity coefficient of 75%, while the coefficients between mid-altitude and high-altitude areas, as well as low-altitude and high-altitude areas, were both14.2%.

Meteorological conditions

Temperature and relative humidity (%RH) varied across villages, with temperature ranging from 14.2 °C to 28.1 °C, both recorded in Magugu Village. Similarly, the lowest and highest %RH was recorded in Magugu and Seloto Villages, at 38% and 86%, respectively, compared to other villages (Table 3). Notably, temperature and %RH demonstrate an inverse relationship.

Discussion

Over the past decade, no new entomological surveys of sandflies have been conducted in the country. In the present study, eight sandfly species were recorded out of ten previously documented (nine were recorded in the work of Minter and Clark et al. 2013 and one originally described by Minter) (Lewis 1982; Clark et al. 2013). Notably, three sandfly species, previously recorded, were not found in this study (*Ph. minteri*, *Ph. guggisbergi*, *Se. clydei*). However, one additional sandfly species (*Se. freetownensis*) was identified. The appearance of this sandfly species and the absence of previously recorded species

Table 2. Species richness and diversity across villages, habitats and altitudinal level (m) a.s.l.

	Localities	Species richness	Abundance	H'	E
Villages	Kigongoni	8	177	0.96	0.461
	Selela	5	312	1.127	0.7
	Migungani B	1	2	0	0
	Magugu	4	93	0.428	0.308
	Loto	1	1	0	0
	Seloto	1	1	0	0
Habitats	Human-wildlife interface	3	41	0.432	0.393
	Farmland	7	295	1.149	0.59
	Peridomicile	7	250	1.1	0.565
Altitudunal range (a.s.l.)	High altitude (> 1500 m)	1	2	0	0
	Mid altitude (1000–1500 m)	7	451	1.079	0.554
	Low altitude (< 1000 m)	7	133	0.799	0.41

H': Shannon diversity index, E: Evenness index.

Table 3. Temperature and Relative humidity range across villages.

Villages	Sandflies abundance	Temperature (°C)		Relative humidity (%)	
		Min.	Max.	Min.	Max.
Magugu	93	14.2	28.1	38	85
Selela	312	23.2	27.3	51	64
Kigongoni	177	21.1	26.5	53	82
Migungani B	2	23.2	25.5	69	82
Loto	1	16.7	21.6	48	79
Seloto	1	16.1	26.1	42	86

could be attributed to variations in geographical locations, collection methods and differences in microhabitats (for example, *Ph. minteri* and *Ph. guggisbergi* are well known as cave-dwelling species), amongst other factors (Savi 2014; Israël et al. 2021).

The samples reveal differences in the composition and abundance of sandflies across habitats. However, the genus *Sergentomyia* dominates, comprising 97.78% of the samples, while the genera *Grassomyia* and *Phlebotomus* account for 0.68% and 1.54%, respectively, the latter being well recognised for its medical significance. The dominance of the genus *Sergentomyia* may reflect its ability to adapt to and tolerate diverse microhabitats (Anjili et al. 2011). Similar phenomena have been reported in Tanzania (Clark et al. 2013) and Chad (Israël et al. 2021). A significantly greater number of male sandflies were captured compared to females, which align with other findings (Senanayake et al. 2015; Talbi et al. 2020; Israël et al. 2021). However, Cazan et al. (2019) collected more females than males. This difference could be due to the difference in trapping methods and the behavioural plasticity of sandfly species, such as phototropism.

The most predominant sandfly species were *Se. antennata* followed by *Se. freetownensis*. The former is recognised as a perennial species with a broad distribution, capable of tolerating various microclimates (Anjili et al. 2011). Furthermore, *Se. freetownensis* exhibits spatial omnipresence, with a constant pattern of occurrence (C = 100%). This observation reflects its ecological prevalence, consistent with Shelford's Law of Tolerance and suggests an adaptive capacity within the study area (Kabbout et al. 2016). Thus, it may indicate the species endemicity in these areas. Additionally, *Se. freetownensis* is known to adapt across the Rift Valley ecosystem in East Africa (Anjili et al. 2011). In contrast, the least dominant species were *Ph. Martini*, followed by *Ph. vansomerenae* and *Gr. squamipleuris*. The latter two species are characterised by limited distribution, with sporadic patterns of occurrence (C = 16%), while *Ph. martini* exhibited an infrequent pattern of occurrence (C = 33%). This suggests that *Ph. vansomerenae* and *Gr. squamipleuris* are rarely encountered species in the area; therefore, in the context of vector epidemiology, *Ph. vansomerenae* may play a very limited role.

Phlebotomus martini and *Ph. vansomerenae* are recognised as competent vectors of visceral leishmaniasis in the neighbouring country of Kenya (Malaria Consortium 2010; Owino et al. 2021). However, the genus *Sergentomyia* has been suspected of being involved in the epidemiology of leishmaniasis, particularly following the detection of *Leishmania* DNA in field-caught *Sergentomyia* sandflies. Notably, *Se. schwetzi* has been identified with *Leishmania donovani* DNA in Kenya (Anjili et al. 2011) and *Leishmania infantum* in Senegal (Senghor et al. 2016). Additionally, *Gr. squamipleuris* (previously classified as *Se.* (*Gr*) *squamipleuris*) has also been found to harbour *Leishmania donovani* DNA in Kenya (Owino et al. 2021), amongst other species. Therefore, the occurrence of *Ph. martini* and *Ph. vansomerenae* in the study areas raises concerns about the risk of leishmaniasis, following the detection of *Leishmania* spp. amastigote in rodents and lizards in the area as recently documented (Samiji et al. 2025). In a nutshell, if the detected parasite is pathogenic to human or accidentally introduced in the area due to migration, tourism activities or other factors, in such a scenario, outbreaks have often

occurred in eastern Africa (Alvar et al. 2021). Furthermore, the detection of *Se. schwetzi* and *Gr. squamipleuris* in the present study is significant, as these species have potential for parasite transmission and, hence, warrant further investigation. Additionally, the over-representation of *Se. antennata* and *Se. freetownensis* may be crucial for determining the epidemiological relevance of these species in the context of leishmaniasis in the area, as discussed in other studies (Ballart et al. 2014; Carvalho et al. 2015).

In the present study, significant differences in species abundance and diversity indices were observed across various habitats, villages and altitudinal ranges. Specifically, the abundance of sandflies was highest in Farmland (295, 50.34%), followed by Peridomicile (252, 43%) and the Human-wildlife interface (HWI) (39, 6.66%). This variation may be attributed to differences in microhabitats, for example, Farmland was characterised by termite hills and rodent burrows, which are known as breeding sites for sandflies. Similarly, the diversity index was highest in Farmland (H' 1.149, R = 7) followed by Peridomicile (H' 1.1, R = 7) and HWI (H' 0.432, R = 3), indicating that farmers working in farmland are more susceptible to contact with vector.

Amongst the villages studied, the Shannon diversity index was highest in Selela (H' 1.127, R = 5) followed by Kigongoni (H' 0.96, R = 8) and Magugu (H' 0.428, R = 4). A community is considered more diverse when it hosts a greater number of species that are evenly abundant (Defilippo et al. 2022). Despite Kigongoni having higher species richness than Selela, it ultimately exhibited lower diversity. This is due to the fact that sandflies species in Selela were more evenly distributed compared to those in Kigongoni. Similarly, across different altitudinal ranges, diversity was higher at mid-altitude (H' 1.079, R = 7) than at low-altitude (H' 0.799, R = 7). The sandfly fauna was not evenly distributed across these categories, with an over-representation of *Se. antennata* and *Se. freetownensis*. A similar phenomenon has been reported in Iran (Arzamani et al. 2018). Importantly, no diversity was observed in Migungani B, Loto, Seloto and the high-altitude area, which presented only a single species and in a low number. This may be influenced by differences in microclimate, as well as environmental features, such as the presence of acacia vegetation and termite hills, amongst others (Kolaczinski et al. 2008; Gálvez et al. 2010; WHO 2022). Defilippo et al. (2022) reported that diversity may change over time and space; therefore, sites need to be compared across different seasons. Unfortunately, no previous studies have been undertaken on the diversity of sandflies in Tanzania, so the present observation needs to be repeated over time and across seasons.

The similarity of sandfly communities across villages, habitats and altitudinal ranges was assessed using Jaccard's similarity coefficient, which revealed a range of 42.8% to 75% amongst habitats. The highest similarity was observed between Farmland and Peridomicile. In contrast, Akhoundi et al. (2013) reported sandfly community similarity coefficients ranging 40% to 100%, which align with our findings. Across altitudinal ranges, Jaccard's coefficient varied from 14.2% to 75%, with high similarity noted between mid-altitude and low-altitude areas. Additionally, amongst villages, Magugu and Selela exhibited a higher similarity of 80% compared to the 62.5% similarity between Kigongoni and Selela and a slight similarity of 50% was observed between Kigongoni and Magugu. Kolaczinski et al. (2008) reported that slight change in temperature and relative

humidity could alter the ecology and development of sandflies. Communities that exhibited greater similarity shared comparable sandfly abundance and common environmental features, such as the presence of acacia vegetation and termite hills. This observation is consistent with other findings suggesting sandflies are mainly associated with the presence of termite hills and acacia vegetation, amongst other factors (Malaria Consortium 2010; Clark et al. 2013).

Like other dipterans, sandflies are climate-sensitive insects affected by temperature and relative humidity, which influence not only their ecology, but also parasite incubation period (Gálvez et al. 2010; Carvalho et al. 2015). In the present study, temperature ranged from 14.2 °C to 28.1 °C and relative humidity ranged from 38% to 85% across the study period and villages. The peak sandflies abundance was observed at temperature between 23.2 °C and 27.3 °C and relative humidity between 51% and 64% in Selela Village. Conversely, in Migungani B Village, which exhibited almost a similar temperature range to Selela, but had higher relative humidity level (69%–82%), sandflies abundance was markedly low. This suggests that temperature, relative humidity and other factors could significantly influence the occurrence and abundance of sandflies. Similar phenomena have also been described in studies conducted in Spain and South America (Ballart et al. 2014; Carvalho et al. 2015).

Conclusions

This study provides comprehensive baseline evidence on the occurrence, species composition and ecological determinants of sandflies, with identified important proven and suspected vectors of the *Leishmania* parasite in certain regions of East Africa, specifically, *Ph. martini*, *Ph. vansomerenae* and *Se. schwetzi*, *Gr. squamipleuris*, respectively. Furthermore, farmland and peridomicile areas were more dominated with sandflies. In this context, farmers working in these agricultural areas are more susceptible to vector contact. Consequently, the detection of these species provides critical information for the health secretariat in the country. Importantly, further research on the vectorial competence, blood meal sources and biting pattern of these species is necessary to assess their role in the epidemiology of the disease in Tanzania. Moreover, the findings presented herein provide information for future research initiatives and underscore the needs for ongoing surveillance.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Ally Samiji: Conceptualisation, Data curation, Formal analysis, Fund acquisition, Investigation, Methodology, Writing-original draft, Writing – review and editing. Jahashi Nzalawahe: Conceptualisation, Methodology, Supervision, Writing – review and editing. Abdul Katakweba: Conceptualisation, Methodology, Resources, Supervision, Writing – review and editing. Ladslaus Mnyone: Conceptualisation, Validation, Methodology, Supervision, Writing – review and editing.

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Data availability

The data used to support the findings of this study are included within the article and in the Supplementary material.

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Supplementary material 1

Location details of each trapping site across villages, and number of Phlebotomine sandflies recorded at each village and spatial pattern

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Data type: docx

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